REMARKS

I. OVERVIEW

Applicants have reviewed and considered the Office Action dated August 3, 2006. Applicants note that claims 1, 4 and 12 are pending in the current application. Claims 2-3, 5-11, and 13-22 have been canceled. Claim 12 is amended. Support for this amendment can be found in the specification as filed, for example, at page 3, lines 22-27; and at page 48, line 21 through page 46, line 24; and claim 11 as originally filed. Since the above amendments merely cancel claims, adopt the Examiner's suggestions, or otherwise remove issues for appeal, Applicants respectfully request entry of the above amendments after final rejection. Applicants aver that no new search is necessitated. The present response is an earnest effort to place all claims in proper form for immediate allowance. Reconsideration and passage to issuance is therefore respectfully requested.

II. OBJECTIONS

A. Claims 8 and 12 stand objected to under 37 C.F.R. § 1.75(c), as allegedly being of improper dependent form for failing to further limit the subject matter of a previous claim. The Examiner further states Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form. The Examiner writes that claims 8 and 12 depend from non-elected claims 5 and 11 respectively.

As an initial matter, claim 8 has been canceled. Applicants have rewritten claim 12 in independent form so that it contains the limitations of previously presented claim 11. Applicants believe they have overcome this objection.

III. ALLEGED NEW MATTER

A. Claim 5 (line 3) allegedly recites new matter as follows: 8-30 contiguous bases'. Applicants' published application, US 2005/0272041 A1, paragraph 007, claims 5 and 9 disclose the range 4-30 contiguous nucleotides. The Examiner states Applicants are required to cancel the new matter in response to this rejection.

While not acquiescing to the Examiner's arguments, Applicants have canceled claims 5 and 9 rendering this bases for this rejection moot.

B. Claim 8 depends upon claim 5, and claim 5 (lines 4-6) allegedly recites new matter as follows: "wherein a nucleotide sequence of said oligonucleotide is obtained by: aligning two or more nucleotide sequences of expansins according to sequence identity to identify a conserved sequence in said expansin sequences". The Examiner continues, there is no basis for these method steps in the specification as originally filed and are required to cancel the new matter in response to this rejection.

While not acquiescing to the Examiner's arguments, Applicants have canceled claims 5 and 8, rendering the bases for this rejection moot.

IV. 35 U.S.C. § 112 - ENABLEMENT

Claims 2-3, 8 and 12 stand rejected under 35 U.S.C. § 112, first paragraph, because the specification, while being enabling, allegedly does not reasonably provide enablement for a polynucleotide that is at least 90% identical to the sequence of SEQ ID NO:1 (claim 2) or a polynucleotide that encodes a polypeptide having at least 90% sequence identity to the sequences of SEQ ID NOS:2-7 (claim 3); or method of identifying a nucleic acid comprising an

oligonucleotide probe of 4-30 contiguous bases of SEQ ID NO:1 (claim 8), or by using an undefined primer of claim 12.

Applicants respectfully disagree. As an initial matter, claims 2-3 and 8 have been canceled. Applicants have amended claim 12 so that it recites "designing a degenerate primer about 4-30 contiguous bases to amplify expansin encoding DNA based upon the N-terminal amino acid sequence of SEQ ID NO:7". Support for this amendment can be found in the specification as filed, for example, at page 3, lines 22-27; at page 48, lines 21 through page 46, line 24; and in originally filed claim 11. Applicants have provided more than enough guidance to allow one skilled in the art to make and use the claimed invention without undue experimentation. Applicants respectfully remind the Examiner that according to MPEP § 2164.04, "A specification disclosure which contains a teaching of the manner and process of making and using an invention in terms which correspond in scope to those used in describing and defining the subject matter sought to be patented must be taken as being in compliance with the enablement requirement of 35 U.S.C. § 112, first paragraph, unless there is a reason to doubt the objective truth of the statements contained therein which must be relied on for enabling support." Applicants respectfully submit that the scope of the claims are commensurate with the specification and therefore meet the enablement requirement.

The Examiner seems to suggest that the claims are not enabled in light of the alleged low sequence homology with expansins isolated from Strawberry, Accession Nos. AAV68447 and W81347. Applicants respectfully submit that the given accession numbers do not correspond to any expansin nucleic acid or protein, rather the sequence submitted under these accession numbers correspond to a Soares fetal heart Homo sapiens cDNA clone and an amino acid sequence for a White Abalone sperm lysin receptor respectively. Copies of the sequence

information in GenBank accession numbers AAV68447 and W81347 are enclosed for the Examiner's convenience. Thus, the Examiner has not met his burden to show Applicants would not be able to identify a number of expansins from various sources including cucumber, rice, and Arabidopsis. Furthermore, the Examiner concedes at page 5 of the Office Action that expansins from these plants are highly conserved in size and sequence similarity (60-87% amino acid sequence identity). Thus, there is no reason to doubt the objective truth of the statements made by Applicants in their specification as to the scope of the invention with regard to being able to isolate expansins using standard techniques and methods. Accordingly, the Examiner has failed to "to explain *why* it doubts the truth or accuracy of any statement in a supporting disclosure and to back up assertions of its own with acceptable evidence or reasoning which is inconsistent with the contested statement" as required by MPEP § 2164.04.

Moreover, the Examiner correctly notes that the article authored Shcherban et al is not prior art and describes the identification of 4 distinct expansin cDNAs in rice and at least 6 in Arabidopsis. Office Action, at page 5. Accordingly, the published journal article by Shcherban et al demonstrates that one of skill in the art, relying on the present disclosure and on knowledge in the art at the time the present application was filed, would be able to identify a variety of expansins having expansin activity. Accordingly, the Specification and published article demonstrate that the methods of the invention are enabled for identifying different expansin nucleotides encoding expansin proteins from various plants.

With regard to the Examiner's comment that claim 12 does not reasonably provide enablement for a polynucleotide identified by using an undefined primer of claim 12, Applicants submit that as applied to amended claim 12, one skilled in the art would know how to make a degenerate primer about 4-30 contiguous bases based on the N-terminal amino acid sequence of

SEQ ID NO:7 and use it to amplify DNA encoding an expansin given the number of examples disclosed in the specification. These examples provide guidance to enable one skilled in the art to use the scope of the invention, a degenerate primer of 4-30 contiguous nucleotides based on SEQ ID NO: 7 of claim 12. Applicants are not required to disclose every species encompassed by their claims. Moreover, enablement is not precluded by necessity for some experimentation such as routine screening. *In re Wands*, 858 F.2d USPQ2d 1400, 1404. The specification sets forth the sequence of SEQ ID NO:7 from which successful primers were obtained, sets forth the length parameters and the minimum number of contiguous bases from SEQ ID NO: 7 and sets forth exemplary, representative primers, for example, at page 48, line 21 through page 46, line 24. Identifying additional degenerate primers would require no more than routine experimentation. The melting temperature of the additional primers can be calculated and used to determine the appropriate annealing and extension temperatures for amplifying expansin DNA. Such calculations are routine and well within the knowledge of one skilled in the art. Therefore, claim 12 should not be limited to a specific primer sequence and Applicants submit that it is commensurate in scope with the disclosure of the claimed invention. Moreover, Applicants' invention is a pioneering invention and therefore is deserving of broad patent protection. Restriction of the invention to a specific primer sequence would unduly limit Applicants' invention and provide inadequate protection from those who would design around Applicants' invention. In light of the above, Applicants respectfully submit that the claims are enabled and in form for allowance.

V. 35 U.S.C. § 112, SECOND PARAGRAPH - CLAIM REJECTIONS

Claims 3 and 12 stand rejected under 35 U.S.C. § 112, second paragraph, as allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The Examiner continues that, claim 3, line 2, recites 'retains biological activity'. The claim is indefinite because it is not clear what activities are encompassed by the phrase biological activity.

Claim 3 has been canceled rendering this rejection moot.

B. Claim 12 is allegedly indefinite because it is not clear how a primer which is a short, single-stranded RNA or DNA segment that functions as the starting point for polymerization of nucleotides, is obtained from a polypeptide sequence of SEQ ID NO:7, unless translated. Claim 12 depends on claim 11, and claim 11 recites 'designing a primer ...based upon SEQ ID NO:7'. The sequence of SEQ ID NO:7 is an amino acid sequence. The Examiner writes it is suggested to amend claim 12 to an independent claim -- and amend claim 12 -- to recite 'designing a degenerate primer ...based upon the N-terminal amino acid sequence of SEQ ID NO:7', to overcome rejection.

Applicants thank the Examiner for the suggestion and accordingly have amended claim 12 to include the adopted language. In light of the above, Applicants respectfully request that the rejection be withdrawn and reconsidered. Applicants respectfully submit that claim 12 is in form for allowance.

VI. DOUBLE PATENTING

The Examiner writes claims 1-4, 8 and 12 are rejected under the judicially created doctrine of double patenting over claims 1-3 of U.S. Patent No. 6,255,466 since the claims, if allowed, would improperly extend the "right to exclude" already granted in the patent.

As an initial matter, claims 2-3 and 8 have been canceled. Applicant is herein submitting a Terminal Disclaimer in compliance with 37 C.F.R. § 1.321(c), which disclaims any term of a patent issuing from this application which would extend beyond the term of U.S. Patent No. 6,255,466. Therefore, Applicant submits that the claims are in proper form for allowance and respectfully request reconsideration and withdrawal of the obviousness-type double patenting rejection.

VII. CONCLUSION

Please charge Deposit Account No. 26-0084 the amount of $65.00 for the Terminal Disclaimer. No other fees or extensions of time are believed to be due in connection with this amendment; however, consider this a request for any extension inadvertently omitted, and charge any additional fees to Deposit Account No. 26-0084.

Reconsideration and allowance is respectfully requested.

Respectfully submitted,

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CUSTOMER NO: **27407**
Attorneys of Record

-pw/bjh-

☐ **1:** AAV68447. Reports vitelline envelop...[gi:55977362] BLink, Links

Features Sequence

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LOCUS       AAV68447                 119 aa            linear   INV 21-MAR-2006
DEFINITION  vitelline envelope sperm lysin receptor [Haliotis sorenseni].
ACCESSION   AAV68447
VERSION     AAV68447.1  GI:55977362
DBSOURCE    accession AY817696.1
KEYWORDS    .
SOURCE      Haliotis sorenseni
  ORGANISM  Haliotis sorenseni
            Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
            Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.
REFERENCE   1  (residues 1 to 119)
  AUTHORS   Gruenthal,K.M. and Burton,R.S.
  TITLE     Genetic diversity and species identification in the endangered
            white abalone (Haliotis sorenseni)
  JOURNAL   Conserv. Genet. 6 (6), 929-939 (2005)
REFERENCE   2  (residues 1 to 119)
  AUTHORS   Gruenthal,K.M. and Burton,R.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-NOV-2004) Marine Biology Research Division, Scripps
            Institution of Oceanography, University of California, San Diego,
            9500 Gilman Drive, La Jolla, CA 92093-0202, USA
COMMENT     Method: conceptual translation.
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Sep 27 2006 15:22:06

1: W81347. Reports zd87d05.r1 Soares...[gi:1392526] Links

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LOCUS       W81347                  265 bp    mRNA    linear   EST 26-JUN-1996
DEFINITION  zd87d05.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
            IMAGE:347625 5' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN
            );; mRNA sequence.
ACCESSION   W81347
VERSION     W81347.1  GI:1392526
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 265)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: mob.REGA+ET
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
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                     /clone_lib="Soares_fetal_heart_NbHH19W"
                     /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
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                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
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adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

ORIGIN

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